

5'	11	AGC	AAG	CAG	GTA	AAC	GAG	CTT	TGT	ACA	AAC	ACA	CAC	AGA	CCA	ACA	CAT	CCG	GGG	56
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	65	ATG	GCT	GTG	TGT	TGC	TAG	AGC	AGA	GGC	TGA	TTA	AAC	ACT	CAG	TGT	GTT	GGC	TCT	110
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	119	CTG	TGC	CAC	TCC	TGG	AAA	ATA	ATG	AAT	TGG	GTA	AGG	AAC	AGT	TAA	TAA	GAA	AAT	164
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	173	GTG	CCT	TGC	TAA	CTG	TGC	ACA	TTA	CAA	CAA	AGA	GCT	GGC	AGC	TCC	TGA	AGG	AAA	218
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	227	AGG	GCT	TGT	GCC	GCT	GCC	GTT	CAA	ACT	TGT	CAG	TCA	ACT	CAT	GCC	AGC	AGC	CTC	272
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	281	AGC	GTC	TGC	CTC	CCC	AGC	ACA	CCC	TCA	TTA	CAT	GTG	TCT	GTC	TGG	CCT	GAT	CTG	326
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	335	TGC	ATC	TGC	TCG	GAG	ACG	CTC	CTG	ACA	AGT	CGG	GAA	TTT	CTC	TAT	TTC	TCC	ACT	380
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

FIGURE 1A

389	GGT	GCA	AAG	AGC	GGA	TTT	CTC	CCT	GCT	TCT	CTT	CTG	416	TCA	CCC	CCG	425	CTC	CTC	434	TCC
443	CCC	AGG	AGG	CTC	CTT	GAT	TTA	TGG	TAG	CTT	TGG	ACT	470	TGC	TTC	CCC	479	GTC	TGA	488	CTG
497	TCC	TTG	ACT	TCT	AGA	ATG	GAA	GAA	GCT	GAG	CTG	GTG	524	AAG	GGA	AGA	533	CTC	CAG	542	GCC
551	ATC	ACA	GAT	AAA	AGA	AAA	ATA	CAG	GAA	GAA	ATC	TCA	578	CAG	AAG	CGT	587	CTG	AAA	596	ATA
605	I	T	D	K	R	K	I	Q	E	E	I	S	Q	K	R	R	L	K	I		
659	GAG	GAA	GAC	AAA	CTA	AAG	CAC	CAG	CAT	TTG	AAG	AAA	632	AAG	GCC	TTG	641	AGG	GAG	650	AAA
	E	E	D	K	L	K	H	Q	H	L	K	K	K	A	L	L	R	E	K		
	659	TTG	CTT	CTA	GAT	GGA	ATC	AGC	AGC	AAA	GAA	CAG	686	GAA	GAG	ATG	695	AAG	AAG	704	CAA
	W	L	L	D	G	I	S	S	G	K	E	Q	E	E	M	K	K	K	Q		

FIGURE 1B

U. S. Dept. of Health, Education, and Welfare
Public Health Service
National Center for Human Genome Research
Washington, D. C. 20540

713	722	731	740	749	758
AAT CAA CAA GAC CAG CAC CAG ATC CAG GTT CTA GAA CAA AGT ATC CTC AGG CTT					
N Q Q D Q H Q I Q V L E Q S I L R L					
767	776	785	794	803	812
GAG AAA GAG ATC CAA GAT CTT GAA AAA GCT GAA CTG CAA ATC TCA ACG AAG GAA					
E K E I Q D L E K A E L Q I S T K E					
821	830	839	848	857	866
GAG GCC ATT TTA AAG AAA CTA AAG TCA ATT GAG CGG ACA ACA GAA GAC ATT ATA					
E A I L K K L K S I E R T T E D I I					
875	884	893	902	911	920
AGA TCT GTG AAA GTG GAA AGA GAA GAA AGA GCA GAA GAG TCA ATT GAG GAC ATC					
R S V K V E R E E R A E E S I E D I					
929	938	947	956	965	974
TAT GCT AAT ATC CCT GAC CTT CCA AAG TCC TAC ATA CCT TCT AGG TTA AGG AAG					
Y A N I P D L P K S Y I P S R L R K					
983	992	1001	1010	1019	1028
GAG ATA AAT GAA GAA AAA GAA GAT GAT GAA CAA AAT AGG AAA GCT TTA TAT GCC					
E I N E E K E D D E Q N R K A L Y A					

FIGURE 1C

1037 1046 1055 1064 1073 1082
 ATG GAA ATT AAA GTT GAA AAA GAC TTG AAG ACT GGA GAA AGT ACA GTT CTG TCT
 M E I K V E K D L K T G E S T V L S
 1091 1100 1109 1118 1127 1136
 TCA ATA CCT CTG CCA TCA GAT GAC TTT AAA GGT ACA GGA ATA AAA GTT TAT GAT
 S I P L P S D D F K G T G I K V Y D
 1145 1154 1163 1172 1181 1190
 GAT GGG CAA AAG TCA GTG TAT GCA GTA AGT TCT AAT CAC AGT GCA GCA TAC AAT
 D G Q K S V Y A V S S N H S A A Y N
 1199 1208 1217 1226 1235 1244
 GGC ACC GAT GGC CTG GCA CCA GTT GAA GTA GAG GAA CTT CTA AGA CAA GCC TCA
 G T D G L A P V E V E E L L R Q A S
 1253 1262 1271 1280 1289 1298
 GAG AGA AAC TCT AAA TCC CCA ACA GAG TAT CAT GAG CCT GTA TAT GCC AAT CCC
 E R N S K S P T E Y H E P V Y A N P
 1307 1316 1325 1334 1343 1352
 TTT TAC AGG CCT ACA ACC CCA CAG AGA GAA ACG GTG ACC CCT GGA CCA AAC TTT
 F Y R P T T P Q R E T V T P G P N F

FIGURE 1D

1361	CAA	GAA	AGG	ATA	AAG	ATT	AAA	ACT	AAT	GGA	CTG	GGT	ATT	GGT	GTA	AAT	GAA	TCC
	Q	E	R	I	K	I	K	T	N	G	L	G	I	G	V	N	E	S
1415	ATA	CAC	AAT	ATG	GGC	AAT	GGT	CTT	TCA	GAG	GAA	AGG	GGA	AAC	AAC	TTC	AAT	CAC
	I	H	N	M	G	N	G	L	S	E	E	R	G	N	N	F	N	H
1469	ATC	AGT	CCC	ATT	CCG	CCA	GTG	CCT	CAT	CCC	CGA	TCA	GTG	ATT	CAA	CAA	GCA	GAA
	I	S	P	I	P	P	V	P	H	P	R	S	V	I	Q	Q	A	E
1523	GAG	AAG	CTT	CAC	ACC	CCG	CAA	AAA	AGG	CTA	ATG	ACT	CCT	TGG	GAA	GAA	TCG	AAT
	E	K	L	H	T	P	Q	K	R	L	M	T	P	W	E	E	S	N
1577	GTC	ATG	CAG	GAC	AAA	GAT	GCA	CCC	TCT	CCA	AAG	CCA	AGG	CTG	AGC	CCC	AGA	GAG
	V	M	Q	D	K	D	A	P	S	P	K	P	R	L	S	P	R	E
1631	ACA	ATA	TTT	GGG	AAA	TCT	GAA	CAC	CAG	AAT	TCT	TCA	CCC	ACT	TGT	CAG	GAG	GAC
	T	I	F	G	K	S	E	H	Q	N	S	S	P	T	C	Q	E	D

FIGURE 1E

1685	GAG	GAA	GAT	GTC	AGA	TAT	AAT	ATC	GTT	CAT	TCC	CTG	CCT	CCA	GAC	ATA	AAT	GAT
	E	E	D	V	R	Y	N	I	V	H	S	L	P	P	D	I	N	D
1739	ACA	GAA	CCG	GTG	ACA	ATG	ATT	TTC	ATG	GGG	TAT	CAG	CAG	GCA	GAA	GAC	AGT	GAA
	T	E	P	V	T	M	I	F	M	G	Y	Q	Q	A	E	D	S	E
1793	GAA	GAT	AAG	AAG	TTT	CTG	ACA	GGA	TAT	GAT	GGG	ATC	ATC	CAT	GCT	GAG	CTG	GTT
	E	D	K	K	F	L	T	G	Y	D	G	I	I	H	A	E	L	V
1847	GTG	ATT	GAT	GAT	GAG	GAG	GAG	GAT	GAT	GAA	GGA	GAA	GCA	GAG	AAA	CCG	TCC	TAC
	V	I	D	D	E	E	E	E	D	E	G	E	A	E	K	P	S	Y
1901	CAC	CCC	ATA	GCT	CCC	CAT	AGT	CAG	GTG	TAC	CAG	CCA	GCC	AAA	CCA	ACA	CCA	CTT
	H	P	I	A	P	H	S	Q	V	Y	Q	P	A	K	P	T	P	L
1955	CCT	AGA	AAA	AGA	TCA	GAA	GCT	AGT	CCT	CAT	GAA	AAC	ACA	AAT	CAT	AAA	TCC	CCC
	P	R	K	R	S	E	A	S	P	H	E	N	T	N	H	K	S	P

FIGURE 1F

2009	2018	2027	2036	2045	2054
CAC AAA AAT TCC ATA TCT CTG AAA GAG CAA GAA AGC TTA GGC AGC CCT GTC					
H K N S I S L K E Q E E S L G S P V					
2063	2072	2081	2090	2099	2108
CAC CAT TCC CCA TTT GAT GCT CAG ACA ACT GGA GAT GGG ACT GAG GAT CCA TCC					
H H S P F D A Q T T G D G T E D P S					
2117	2126	2135	2144	2153	2162
TTA ACA GCT TTA AGG ATG AGA ATG GCA AAG CTG GGA AAA AAG GTG ATC TAA GAG					
L T A L R M R M A K L G K K V I *					
2171	2180	2189	2198	2207	2216
TTG TAC CAC CTA TAT AAA CAT CCT TTG AAG AAG AAA CTA AGA AGC ATT TGC AAA					
2225	2234	2243	2252	2261	2270
TTT CTC TTC TGG ATA TTT TGT TTA TTT TTT CTG AAG TCC AAA AAA TTA TCA TTA					
2279	2288	2297	2306	2315	2324
CAG TGT ACC ATA TTA AGC CAT GTG AAT AAG TAG TAG TCA TTA TTT GTG AAA AAT					

FIGURE 1G

2333	2342	2351	2360	2369	2378
TCC CAA AAA	GCT GGG GAA AAC AAA	TGT GTA ACT TTT CCA GTT ACT	TGA CAC GAT		
---	---	---	---	---	---
2387	2396	2405	2414	2423	2432
TCA GTG GGG	GAA AAC CAG CAT TTT TTA	TTC TAT TGA TAC CAA AGC	ATT TCT AAT		
---	---	---	---	---	---
2441	2450	2459	2468	2477	
AAG AGC TTG	TTA AAT TTA AGA ATA AAG	TTA TTT AAA ATA AAA AAA	AAA A 3'		
---	---	---	---	---	---

FIGURE 1H

[illegible]

FIGURE 2A

335	344	353	362	371	380
TCCT CCT	CAA AGG AAA GAA AAC AGG GCA TGC GCT TGT	TGG CAA AAC	GCA GGG CCG		
S P Q R K E N R A C A C W Q N A G P					
389	398	407	416	425	434
GCT CCC AAA AAC CCC ATG TGT GTA CGA TTA AAA GTT GGC CGT CCC					TCC
A P K N P M C V R L K V G R P Q A S					
443	452	461	470	479	488
CAG CGC AAA CTT AAA GAG ACA GGG CTT TGC TGA AAA CCA AAC ATG GGC CAG CTG					
Q R K L K E T G L C *					
497	506	515	524	533	542
GGC TTT TTA ACA ACC TAG AGA CTT TCC GGA GCT GCC TGG AAC AGA GCC TGC GGG					
551	560	569	578	587	596
AAA CGG GGC TTG CCA GAG ACA CTC ACA GTT TCC TGC TTC ATG GCC TGT TTT GGT CCC					
605	614	623	632	641	650
CTA AGA ATC TCC ACA TCA TTG TCT TTC TTG TGC CTT TTC CTT GGT GAG CAA CAG					
659	668	677	686	695	704
AAA GGG AAG GGT TCC AAG CCT CTA AAA ATG TGC TTT GTG ATC AGG AGT GCG CTC					

FIGURE 2B

713	CAA	ACC	AAA	TAC	GCG	CGC	TGC	CCT	TTC	GAG	GCC	AGT	GAG	CTC	AGC	CTC	CAA	GGC	758
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	767	TTT	AAA	GCC	ACA	TTT	CAG	CAA	GAG	AAA	GCG	CTG	AGA	GCT	CGC	AGG	TTC	ATT	AAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	821	GAA	GGC	AAA	GCA	CTG	GTG	TCT	CTC	CTT	AGA	AAA	GTA	GGT	TTC	TTC	GCT	TGA	TGT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	875	AGA	CTG	GCT	TGC	TTT	GAT	TTT	TAG	TGA	AGG	GAA	TGT	ACG	TAA	AAC	AAA	ATA	GGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	929	CIT	GGC	TGG	TCA	AAG	GAG	ACA	AGC	AGG	ATG	GAT	GGA	TGG	ATG	GAT	GGA	TGG	ATG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	983	TAT	GGA	TGA	ATA	GAT	AGA	TGG	TGT	TTG	CAT	GTA	AAT	TGC	AGA	GAA	AAC	AAA	ACC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1037	AAA	GCT	GAT	TGG	AAA	CAA	TTA	ATT	GTG	GGT	GTC	TGA	GGG	GGA	AGG	TCG	CAG	CTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

FIGURE 2C

1091	TGG	GCA	GCT	TTG	AGA	AGC	GGT	ACA	AGA	GTT	CTG	TGC	1118	1127		1136
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1145	AGC	CAG	CCA	GTG	CAT	TTA	TTT	TAA	GCT	CTT	AGA	AGC	1172	1181		1190
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1199	TGC	GTG	ACC	CCT	GAG	ATG	GGT	CCA	CGC	ATC	TCT	CTA	1226	1235		1244
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1253	GGA	TAC	TGG	ACT	CGT	GCC	TCT	GCG	CCC	ATT	CTC	TTC	1280	1289		1298
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1307	TTT	AAT	TTC	ACT	TTC	TGA	TCA	CGG	TAC	GTC	CAT	AAA	1334	1343		1352
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1361	TGA	AGT	ATT	CTT	TTT	TGT	AAT	CGT	TTT	TTT	TAG	AAG	1388	1397		1406
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1415	GCT	ACC	AAT	AAT	GAG	AAA	AAA	AAA	AAA	AAA	AAA	AAA				
--	--	--	--	--	--	--	--	--	--	--	--	--				

FIGURE 2D

5'	9			18			27			36			45			54		
CAA	CCA	GGG	TCA	GGC	TGT	GCT	CAC	AGT	TTC	CTC	TGG	CGG	CAT	GTA	AAG	GCT	CCA	
CAA	AGG	AGT	TGG	GAG	TTC	AAA	TGA	GGC	TGC	TGC	GGA	CGG	CCT	GAG	GAT	GGA	CCC	
CAA	GCC	CTG	GAC	CTG	CCG	AGC	GTG	GCA	CTG	AGG	CAG	CGG	CTG	ACG	CTA	CTG	TGA	
GGG	AAA	GAA	GGT	TGT	GAG	CAG	CCC	CGC	AGG	ACC	CCT	GGC	CAG	CCC	TGG	CCC	CAG	
CCT	CTG	CCG	GAG	CCC	TCT	GTG	GAG	GCA	GAG	CCA	GTG	GAG	CCC	AGT	GAG	GCA	GGG	
CTG	CTT	GGC	AGC	CAC	CGG	CCT	GCA	ACT	CAG	GAA	CCC	CTC	CAG	AGG	CCA	TGG	ACA	
GGC	TGC	CCC	GCT	GAC	GGC	CAG	GGT	GAA	GCA	TGT	GAG	GAG	CCG	CCC	CGG	AGC	CAA	

FIGURE 3A

[illegible]

FIGURE 3B

711	GAG	CTA	GAG	CTG	CTC	AAC	AAT	GAG	CTG	CTC	AAG	CAG	AAG	CGG	CAG	ATC	GAG	ACG	756
	E	L	E	L	L	N	N	E	L	L	K	Q	K	R	Q	I	E	T	
720	CTG	CTG	CTG	CTG	CTG	AAC	AAT	GAG	CTG	CTC	AAG	CAG	AAG	CGG	CAG	ATC	GAG	ACG	
	L	E	L	L	L	N	N	E	L	L	K	Q	K	R	Q	I	E	T	
729	CTG	CAG	CAG	CTG	CTG	GAG	GTG	GAC	GGC	GGC	ATT	GTG	AGC	GAG	GTG	AAG	CTG	CTG	810
	L	Q	Q	L	L	V	E	D	G	G	I	V	S	E	V	K	L	L	
738	CGC	AAG	GAG	AGC	CGC	AAC	ATG	AAC	TCG	CGG	GTC	ACG	CAG	CTC	TAC	ATG	CAG	CTC	864
	R	K	E	S	R	N	M	N	S	R	V	T	Q	L	Y	M	Q	L	
747	CTG	CAC	GAG	ATC	ATC	CGC	AAG	CGG	GAC	AAC	GCG	TTG	GAG	CTC	TCC	CAG	CTG	GAG	918
	L	H	E	I	I	R	K	R	D	N	A	L	E	L	S	Q	L	E	
756	AAC	AGG	ATC	CTG	AAC	CAG	ACA	GCC	GAC	ATG	CTG	CAG	CTG	GCC	AGC	AAG	TAC	AAG	972
	N	R	I	L	N	Q	T	A	D	M	L	Q	L	A	S	K	Y	K	
765	GAG	CTG	CAG	CAC	AAG	TAC	CAG	CAC	CTG	GCC	ACA	CTG	GCC	CAC	AAC	CAA	TCA	GAG	1026
	D	L	E	H	K	Y	Q	H	L	A	T	L	A	H	N	Q	S	E	

FIGURE 3C

1035	ATC	ATC	GCG	CAG	C'TT	GAG	GAG	CAC	TGC	CAG	AGG	GTG	CCC	TCG	GCC	AGG	CCC	GTC
1044	I	I	A	Q	L	E	E	H	C	Q	R	V	P	S	A	R	P	V
1053	1089	1089	CAG	CCA	CCC	CCC	GCT	GCC	CCG	CCC	CGG	GTC	TAC	CAA	CCA	CCC	ACC	TAC
1062	1098	1098	P	Q	P	P	A	A	P	P	R	V	Y	Q	P	P	T	Y
1071	1107	1107	1143	ATC	ATC	AAC	CAG	ATC	TCT	ACC	AAC	GAG	ATC	CAG	AGT	GAC	CAG	AAC
1080	1116	1116	1152	CGC	ATC	AAC	CAG	ATC	TCT	ACC	AAC	GAG	ATC	CAG	AGT	GAC	CAG	AAC
1134	1170	1170	1188	R	I	I	N	Q	I	S	T	N	E	I	Q	S	D	Q
1179	1224	1224	1233	1197	CTG	CCA	CCC	CCT	CTG	CCC	ACT	ATG	CCC	ACT	CTC	ACC	AGC	CTC
1242	1269	1269	1278	V	L	P	P	L	P	T	M	P	P	T	L	T	S	L
1287	1296	1296	1305	ACC	GAC	AAG	CCG	TCG	GGC	CCA	TGG	AGA	GAC	TGC	CTG	CAG	GCC	CTG
1341	1350	1350	1350	T	D	K	P	S	G	P	W	R	D	C	L	Q	A	L
1350	1350	1350	1350	CAC	GAC	ACC	AGC	TCC	ATC	TAC	CTG	GTG	AAG	CCG	GAG	AAC	ACC	AAC
1350	1350	1350	1350	H	D	T	S	S	I	Y	L	V	K	P	E	N	T	N
1350	1350	1350	1350															

FIGURE 3D

	1359	CAG GTG TGG TGC GAC CAG AGA CAC GAC CCC GGG GGC TGG ACC GTC ATC CAG AGA	1368	1377	1386	1395	1404
	Q V W C D Q R H D P G G W T V I Q R						
	1413	CGC CTG GAT GGC TCT GTT AAC TTC TTC AGG AAC TGG GAG ACG TAC AAG CAA GGG	1422	1431	1440	1449	1458
	R L D G S V N F F R N W E T Y K Q G						
	1467	TTT GGG AAC ATT GAT GGC GAA TAC TGG CTG GGC CTG GAG AAC ATT TAC TGG CTG	1476	1485	1494	1503	1512
	F G N I D G E Y W L G L E N I Y W L						
	1521	ACG AAC CAA GGC AAC TAC AAA CTC CTG GTG ACC ATG GAG GAC TGG TCC GGC CGC	1530	1539	1548	1557	1566
	T N Q G N Y K L L V T M E D W S G R						
	1575	AAA GTC TT'T GCA GAA TAC GCC AGT TTC CGC CTG GAA CCT GAG AGC GAG TAT TAT	1584	1593	1602	1611	1620
	K V F A E Y A S F R L E P E S E Y Y						
	1629	AAG CTG CGG CTG GGC CGC TAC CAT' GGC AAT GCG GGT GAC TCC TTT ACA TGG CAC	1638	1647	1656	1665	1674
	K L R L G R Y H G N A G D S F T W H						

FIGURE 3E

1. If the first and last bases are the same, the sequence is a repeat.
 2. If the first and last bases are different, the sequence is a mutation.

1683	1692	1701	1710	1719	1728
AAC GGC AAG CAG TTC ACC ACC CTG GAC AGA GAT CAT GAT GTC TAC ACA GGA AAC					
N G K Q F T T L D R D H D V Y T G N					
1737	1746	1755	1764	1773	1782
TGT GCC CAC TAC CAG AAG GGA GGC TGG TGG TAT AAC GCC TGT GCC CAC TCC AAC					
C A H Y Q K G G W Y N A C A H S N					
1791	1800	1809	1818	1827	1836
CTC AAC GGG GTC TGG TAC CGC GGC GGC CAT TAC CGG AGC CGC TAC CAG GAC GGA					
L N G V W Y R G G H Y R S R Y Q D G					
1845	1854	1863	1872	1881	1890
GTC TAC TGG GCT GAG TTC CGA GGA GGC TCT TAC TCA CTC AAG AAA GTG GTG ATG					
V Y W A E F R G G S Y S L K K V M					
1899	1908	1917	1926	1935	1944
ATG ATC CGA CCG AAC CCC AAC ACC TTC CAC TAA GCC AGC TCC CCC TCC TGA CCT					
M I R P P N P N T F H *					
1953	1962	1971	1980	1989	1998
CTC GTG GCC ATT GCC AGG AGC CCA CCC TGG TCA CGC TGG CCA CAG CAC AAA GAA					

FIGURE 3F

.....
 if it had and the if ..
 if had and then had

2007	2016	2025	2034	2043	2052
CAA CTC CTC ACC AGT TCA TCC TGA GGC TGG GAG GAC CGG GAT GCT GGA TTC TGT					
2061	2070	2079	2088	2097	2106
TTT CCG AAG TCA CTG CAG CGG ATG ATG GAA CTG AAT CGA TAC GGT GTT TTC TGT					
2115	2124	2133	2142	2151	2160
CCC TCC TAC TTT CCT TCA CAC CAG ACA GCC CCT CAT GTC TCC AGG ACA GGA CAG					
2169	2178	2187	2196	2205	2214
GAC TAC AGA CAA CTC TTT CTT TAA ATA AAT TAA GTC TCT ACA ATA AAA ACA CAA					
2223	2232	2241	2250	2259	2268
CTG CAA AGT ACC TTC ATA ATA TAC ATG TGT ATG AGC CTC CCT TGT GCA CGT ATG					
2277	2286				
TGT ATA GCA CAT ATA TAT GG 3'					

FIGURE 3G

NORTHERN ANALYSIS OF SEQ ID NO:3

Category	cDNAs	Libraries	Abund	%Abund
Cardiovascular	270162	15/72	19	0.0070
Connective	147886	15/54	26	0.0176
Digestive	514430	33/151	54	0.0105
Embryonic	107325	2/23	2	0.0019
Endocrine	233587	7/63	8	0.0034
Exocrine	255105	17/64	28	0.0110
Female Reprod	445078	25/113	48	0.0108
Male Reprod	453150	32/118	44	0.0097
Germ Cells	46185	1/5	9	0.0195
Hemic/Immune	701709	8/166	8	0.0011
Liver	110945	2/34	2	0.0018
Musculoskeletal	162794	10/50	16	0.0098
Nervous	973795	25/221	45	0.0046
Pancreas	111757	3/25	19	0.0170
Respiratory	407942	14/95	21	0.0051
Sense Organs	25346	1/10	1	0.0039
Skin	72110	1/15	1	0.0014
Stomatognathic	14025	0/11	0	0.0000
Unclass./Mixed	150146	6/19	31	0.0206
Urinary Tract	287931	12/66	22	0.0076
Totals	5491408	229/1375	404	0.0001

Legend: The first column presents the category (cell tissue or organ), the second column, the number of cDNAs sequenced for that category; the third column, description of the tissue; the fourth column, absolute abundance of the transcript; and the fifth column, percent abundance of the transcript (abundance divided by the number of clones)

FIGURE 4

Differential Expression of SEQ ID NO:3 in Pancreas

Found in:

<u>Library</u>	<u>cDNAs</u>	<u>Description</u>	<u>Abund</u>	<u>%Abund</u>
PANCTUP01	1205	pancreatic tumor, TIGR	1	0.0830
PANCTUP032	2651	pancreas tumor, adenoCA, 3' CGAP	17	0.0751
PANCTUT021	1545	pancreatic tumor, anaplastic CA, 45F	1	0.0087

Not found in:

<u>Library</u>	<u>cDNAs</u>	<u>Description</u>
PANCDIR02	2023	pancreas, type I diabetes, 43F, RP
PANCDIT01	1741	pancreas, type I diabetes, 15M
PANCN0T23	3919	pancreas, type I diabetes, 43F
PANCDIT03	688	pancreas, type II diabetes, 57M
PANCNOE02	2834	pancreas, 8M, 5RP
PANCNOP03	589	pancreas, 34F, WN
PANCNOP05	373	pancreas, CGAP
PANCN0T01	4452	pancreas, 29M
PANCN0T0411135		pancreas, 5M
PANCN0T05	6788	pancreas, 2M
PANCN0T07	6991	pancreas, fetal, 23wM
PANCN0T08	3901	pancreas, pancreatitis, mw/adenoCA, 65F, m/PANCTUT01
PANCN0T15	3638	pancreas, islet cell hyperplasia, 15M
PANCN0T16	2994	pancreas, aw/Patau's, fetal, 20wM
PANCN0T17	4034	pancreas, mw/neuroendocrine CA, aw/node, liver mets, 65F
PANCN0T19	3772	pancreas, 8M
PANCN0T21	3841	pancreas, 8M
PANCN0T22	1356	pancreas, 17F

Legend: The first range shows the expression of SEQ ID NO:3 in pancreas. SEQ ID NO:3 is differentially expressed in pancreatic tumors and diagnostic of that condition. The second range shows that the sequence is not expressed in type I and II diabetes, in pancreatitis, or in metastatic liver cancer.

Where present, the first column presents the library name, the second column, the number of cDNAs sequenced for that library; the third column, description of the tissue; the fourth column, absolute abundance of the transcript; and the fifth column, percent abundance of the transcript (abundance divided by the number of clones)

Note: Normalized and subtracted tissues, which have high abundance transcripts removed before sequencing, were not considered in this analysis.

FIGURE 5